Such an embodiment is illustrated in Figures 1 and 2. Fig. 1 illustrates schematically the operation of an embodiment of a method in accordance with the present invention at an intermediate stage after the addition of aptamers to an aliquot with a sample being analyzed. In this example, we are performing a quantitative assay for target proteins A and B, namely items **106** and **107** respectively, that occur in low abundance in a sample contained in a region **101**, which is here a vessel such as an Eppendorf tube. Also in the sample in Fig. 1 are a number of proteins that are not of interest, namely X and Y, items **102** and **103** ~~and **104**~~, respectively. Also placed in the region is an aptamer **104** that is specific for protein A and an aptamer **105** that is specific for protein B. These aptamers are present in relatively larger abundance in the region than the target proteins, with the result that substantially all of proteins A and B in the region form complexes with their respective aptamer, and excess uncomplexed quantities of each of the aptamers for each of the target proteins remain in the sample.

Support for this amendment is found in Fig. 1, and represents obvious error in that the description, and Fig. 1, make clear that items X and Y, examples of target molecules, are correctly labeled as **102** and **103**, respectively, in Fig. 1, and erroneously described as numbers **103** and **104** in the text on pp. 10-21.

Amendments to the Claims

Please amend claims 1, 2, 29-32 and 45 as indicated below:

1. (currently mended) A method for quantitatively assaying one or more target molecules in a first sample, comprising:
   (a) adding to the first sample, a preparation of a nucleic acid aptamer specific for each target molecule;
   (b) allowing substantially all of the target molecules in the first sample to bind with the aptamer;
   (c) separating unbound aptamer from the first sample by contacting the sample of step (b) with immobilized ligands, thereby binding the ligands to unbound aptamer, so as to recover a second sample of aptamer bound to target molecules; and
   (d) using a quantitative replicative procedure comprising a replicative polymerase reaction to determine a quantity of aptamer specific for each target molecule in the second sample and therefore related to the concentration of target molecule in the first sample.